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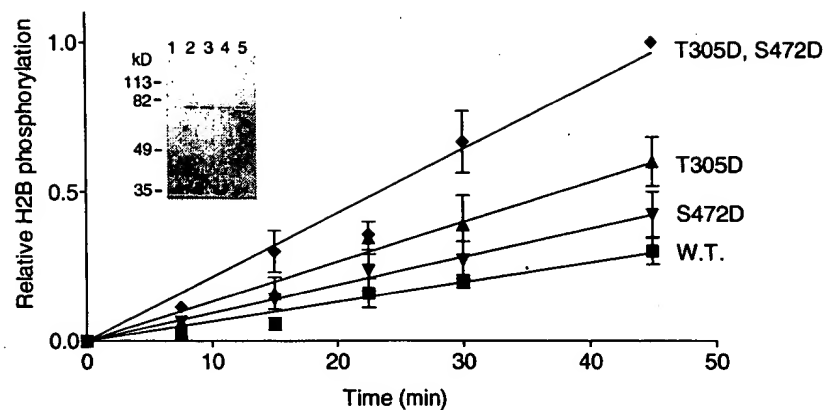
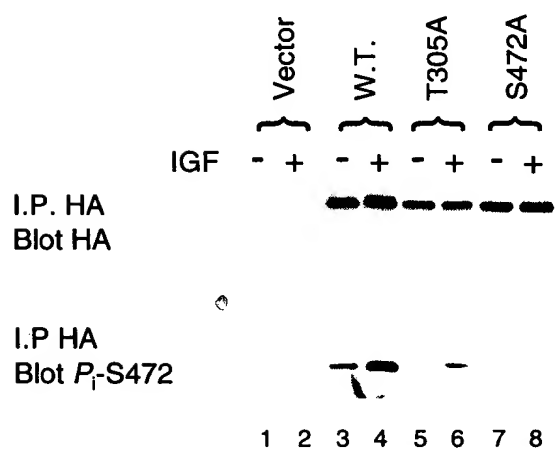
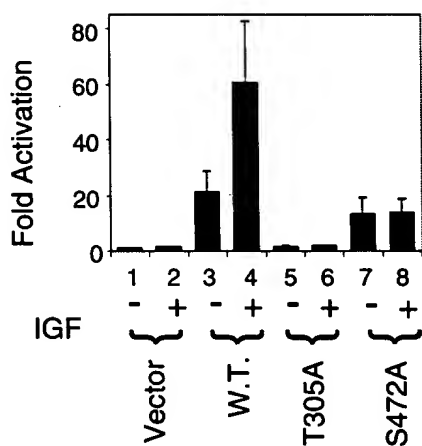


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 1 GGGAGTCATCATGAGCGATGTTACCATTGTGAAAGAAGGTTGGGTTCCAGAAGAGGGGAGA  
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 61 ATATATAAAAACTGGAGGCCAAGATACTTCCTTTTGAAGACAGATGGCTCATTTCATAGG  
 Y K E K P Q D V D L P Y P L N N F S V A 57  
 121 ATATAAAGAGAAACCTCAAGATGTGGATTACCTTATCCCCTCAACAACCTTTTCAGTGGC  
 K C O L M K T E R P K P N T F I I R C L 77  
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 Q W T T V I E R T F H V D T P E E R E E 97  
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 W T E A I Q A V A D R L Q R O E E E R M 117  
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 N C S P T S Q I D N I G E E E M D A S T 137  
 361 GAATTGTAGTCCAACCTTCACAAATTGATAATATAGGAGAGGAAGAGATGGATGCCTCTAC  
 T H H K R K T M N D F D Y L K L L G K G 157  
 421 AACCCATCATAAAGAAAGACAATGAATGATTTTGACTATTTGAAACTACTAGGTAAAGG  
 T F G K V I L V R E K A S G K Y Y A M K 177  
 481 CACTTTTGGGAAAGTTATTTTGGTTCGAGAGAAGGCAAGTGGAAAATACTATGCTATGAA  
 I L K K E V I I A K D E V A H T L T E S 197  
 541 GATTCTGAAGAAAGAAGTCATTATTGCAAAGGATGAAGTGGCACACACTCTAACTGAAAG  
 R V L K N T R H P F L T S L K Y S F Q T 217  
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 K D R L C F V M E Y V N G G E L F F H L 237  
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 721 GTCGAGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATGGTGCAGAAATTGTCTC  
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 781 TGCCTTGGACTATCTACATTCCGGAAGATTGTGTACCGTGATCTCAAGTTGGAGAATCT  
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 1321 AGAATTTACAGCTCAGACTATTACAATAACACCACCTGAAAAATATGATGAGGATGGTAT  
 D C M D N E R R P H F P O F S Y S A S G 477  
 1381 GGACTGCATGGACAATGAGAGGCGGCCGATTTCCCTCAATTTTCTACTCTGCAAGTGG  
 R E 479  
 1441 ACGAGAATAAGTCTCTTTCATTCTGCTACTTCACTGTCTCTTCAATTTATTACTGAAAA  
 1501 TGATTCTGACATCACCAGTCTTAGCTCTTACACATAGCAGGGGCA

Figure 1

Figure 2

|         |   |       |
|---------|---|-------|
| Akt-1 : | MSDVAIVRESGMLHKGGEYIKTMRRERYFLBNDCGTFIGYKERPDQVLCREAEIINNPSVAQCQLMKTERERENTFIIRCLQMTTVIERPHW  | : 90  |
| Akt-2 : | MNEVSVINEGSMHKGGEYIKTMRRERYFLBNDCGTFIGYKERPEAPDCTPELINNPSVAECQLMKTERERENTFVIRCLQMTTVIERPHW    | : 90  |
| Akt-3 : | MSDVAIVRESGMLHKGGEYIKTMRRERYFLBNDCGTFISYKERPDQVLDPEYELINNPSVAQCQLMKTERERENTFIIRCLQMTTVIERPHW  | : 89  |
| <br>    |   |       |
| Akt-1 : | ETFEEREEMTTSICQVADGLKKQE--EEEMDFRS6SPSDNSGAEEMEVSILAKPKHRRVTMMNEFEYLKLLGKGTGPKVILVKEKATGRXYAM | : 178 |
| Akt-2 : | DSFDEREEMPRALCWANSLKORAPGEDDMDYKCGSPSDSSSTTEEMEVAVSERAKAKVTMMNDFDXLLKLLGKGTGPKVILVREKATGRXYAM | : 180 |
| Akt-3 : | DTFEEREEMTTSICQVADGLKKQE--EERQNCSPTSQILNIGEEEDDASTTHRK-RKTMNDFDXLLKLLGKGTGPKVILVREKATGRXYAM   | : 176 |
| <br>    |   |       |
| Akt-1 : | KILNKEVIAKDEVAHTITENRVLQMSRHPPFTALKYSFQTHDRLCFVMEYANGGELFFHLSPERVPSEDPRPFYGAETVSALDYLHSEK     | : 268 |
| Akt-2 : | KILNKEVIAKDEVAHTITENRVLQMSRHPPFTALKYAFQTHDRLCFVMEYANGGELFFHLSPERVPSETEPRPFYGAETVSALDYLHSE-R   | : 269 |
| Akt-3 : | KILNKEVIAKDEVAHTITENRVLQMSRHPPFTALKYSFQTKORLCFVMEYVNGGSELFFHLSPERVPSEDPTRPFYGAETVSALDYLHSE-G  | : 265 |
| <br>    |   |       |
| Akt-1 : | NQVYRDLKLENMLDKDGHKIKITDPGLCKNEGTIKIGATMKTFQGTPEYLAPEVLEDNDYGRAVIMMGLGVVMYEMMCGRLPFFYMQDHEKLF | : 358 |
| Akt-2 : | DQVYRDLKLENMLDKDGHKIKITDPGLCKNEGTISDGATMKTFQGTPEYLAPEVLEDNDYGRAVIMMGLGVVMYEMMCGRLPFFYMQDHEKLF | : 359 |
| Akt-3 : | KIVYRDLKLENMLDKDGHKIKITDPGLCKNEGTILATMKTFQGTPEYLAPEVLEDNDYGRAVIMMGLGVVMYEMMCGRLPFFYMQDHEKLF   | : 355 |
| <br>    |   |       |
| Akt-1 : | ELILMEEIRFPFRLGPEAKSLLSLLKKNDKORLGGGSEDAKEIMCHRPFACTVMCHVYENKLSPPFPQVTSSETDTRYPFDEEFTACTMIT   | : 448 |
| Akt-2 : | ELILMEEIRFPFRLGPEAKSLLSLLKKNDKORLGGGSPDANEVMEHRPFLSINMQDMVQNNLPEEPFQVTSSEVDTRYPFDEEFTACTIT    | : 449 |
| Akt-3 : | ELILMEDIKRFPFRLGSDAKSLLSLLINDENKRLGGGSDDAKEIMRSEFSEVNMQDMVDKNI VEPFEPQVTSSETDTRYPFDEEFTACTIT  | : 445 |
| <br>    |   |       |
| Akt-1 : | ITPFDQDGS--MEQVLSERRPHFPQFSYASGTA   | : 480 |
| Akt-2 : | ITPFDQDGS--IGLLELDQFTHFPQFSYASGRE   | : 481 |
| Akt-3 : | ITPFEKYNEDGDDQMNERNRPHFPQFSYASGRE   | : 479 |

**A****B****C****Figure 3**

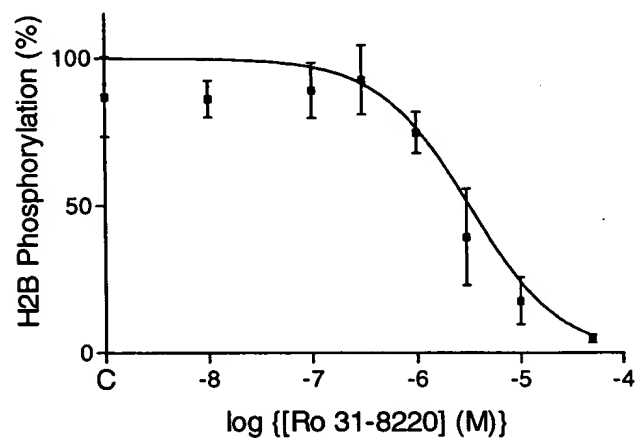
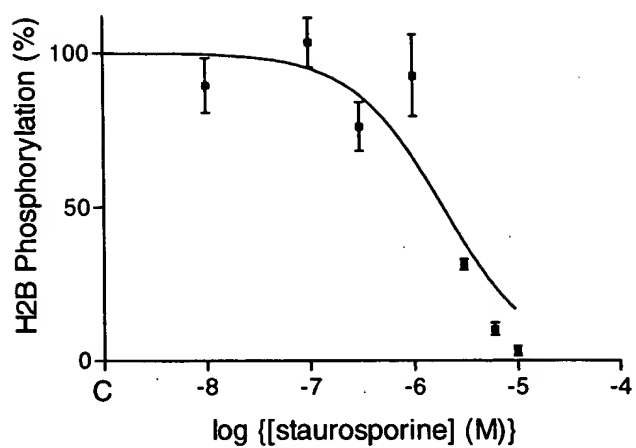
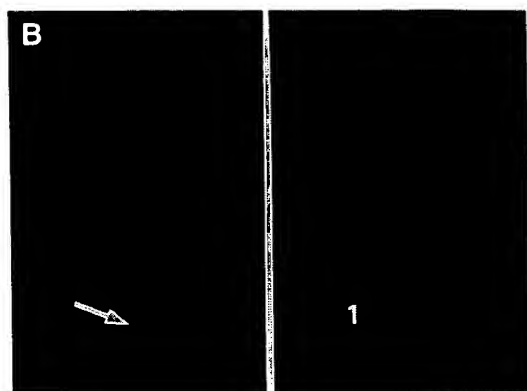
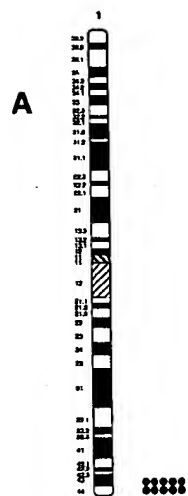
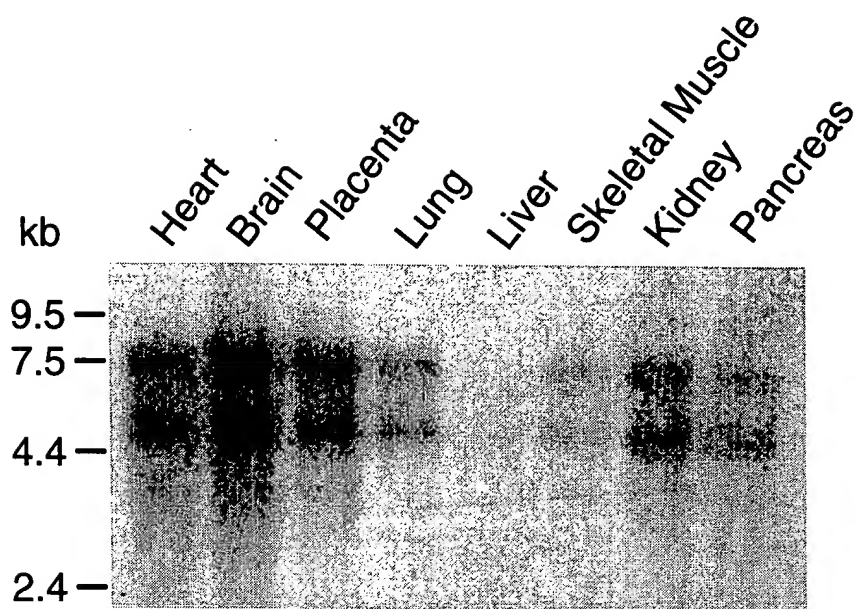


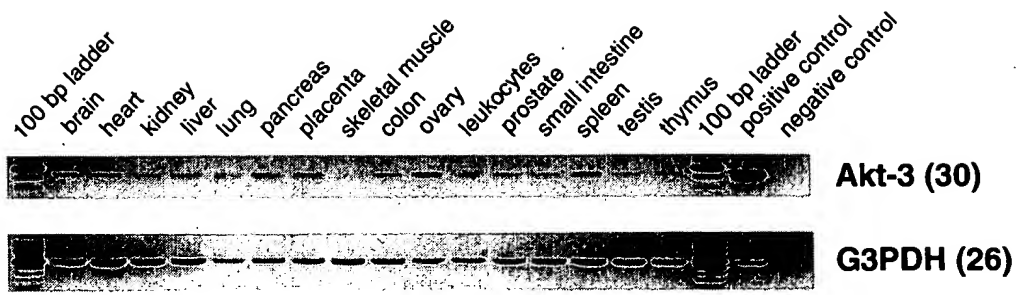
Figure 4.



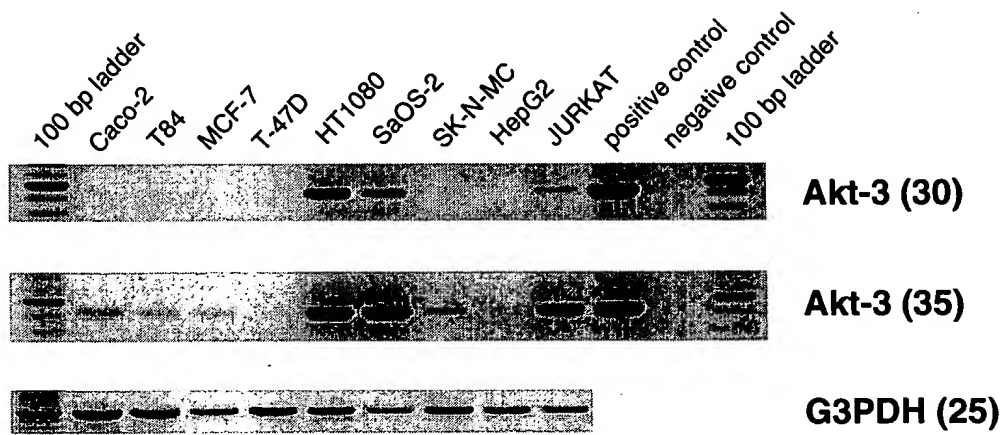
**Figure 5**



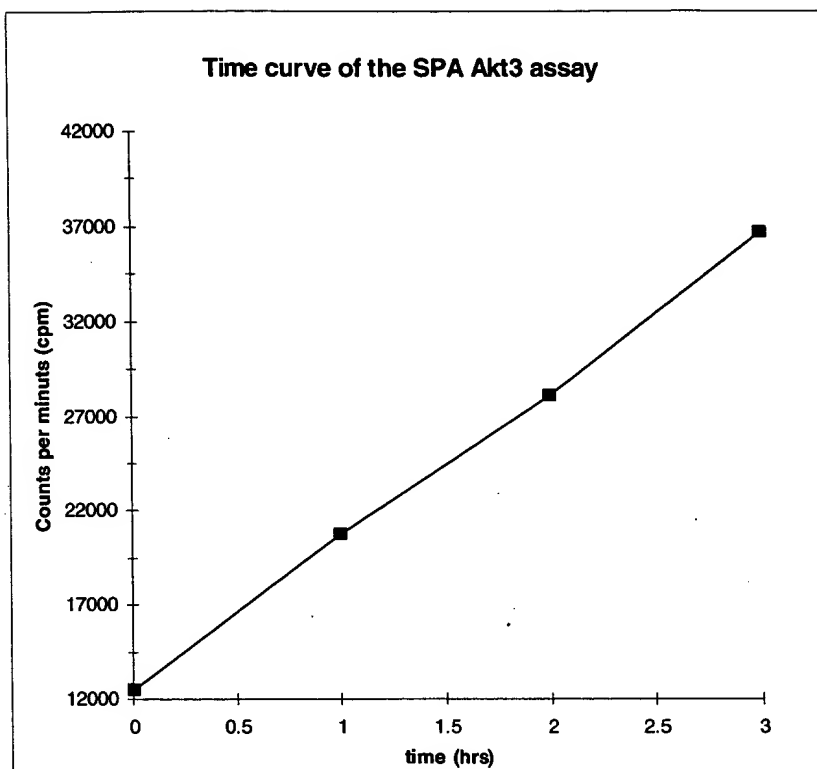
**Figure 6A**



**Figure 6B**

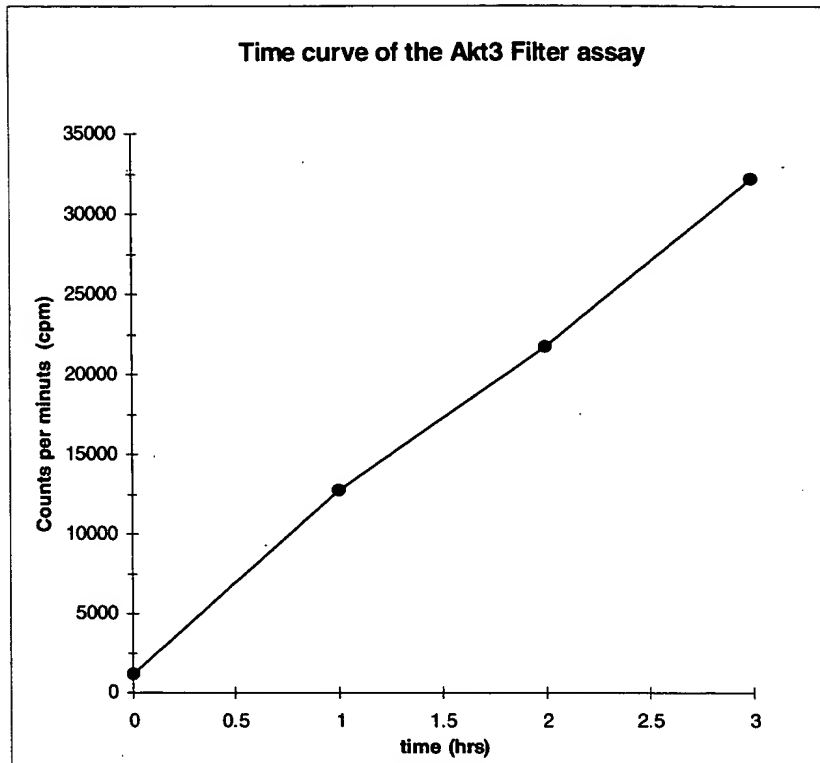


**Figure 6C**



**Figure 7**





**Figure 8**

# FIG. 2

Akt-1 : MSDVAIVKEGWLHKGGEYIKTWRRPRYELLKNDGTFIGYKERPDVDQREAPLNNFSAQCQLMKTERPRPNTFIIRCLQWTTVIERTFHV : 90  
Akt-2 : MNEVSVIKEGWLHKGGEYIKTWRRPRYELLKSDGSFIGYKERPEAPDQTLPLNNFSAECQLMKTERPRPNTFIIRCLQWTTVIERTFHV : 90  
Akt-3 : MSDVTIKEGWVQKRGEYIKTWRRPRYELLKTDGSFIGYKERPODVDLP-YPLNNFSAVKCOLMKTERPKPNTFIIRCLQWTTVIERTFHV : 89

Akt-1 : ETPEEREWEWTIAQITVADGKKQEE--EEEMDFRSGSPDSNSGAEEEMVSLAKPKHRTVMNPEYLLKLGKGTGKGVILVKEKATGRYYAM : 178  
Akt-2 : DSPDEREEWMRAIQMWANSIKQAPGEDPMDYKCGSPDSSTTEEMEVAVSKAPAKVTMNDPDYLLKLGKGTGKGVILVREKATGRYYAM : 180  
Akt-3 : DTPEEREWEWTIAQIAVADRILQRE--EERVNCSPTSQIDNIGEEMDASTTHK-RKTMNDPDYLLKLGKGTGKGVILVREKASGKYYAM : 176

Akt-1 : KILKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLSRERVFSEDRRARFYGAIEVSALDYLHSEK : 268  
Akt-2 : KILPKEVIAKDEVAHTVTESRVLQNTRHPFLTALKYAFQTHDRLCFVMEYANGGELFFHLSRERVFTEERARFYGAIEVSALDYLHS-R : 269  
Akt-3 : KILKKEVIVAKDEVAHTLTENRVLQNSRHPFLTALKYSFQTKDRLCFVMEYANGGELFFHLSRERVFSEDRTIRFYGAIEVSALDYLHS-G : 265

Akt-1 : NVVYRDLKLENMLDKDGHIKITDFGLCKEGIKDGATMKTCGTPEYLAPEVLEDNDYGRAVDWWGLGVVMYEMMCGRLPFYQNDHEKLF : 358  
Akt-2 : DVVYRDIKLENMLDKDGHIKITDFGLCKEGISDGATMKTCGTPEYLAPEVLEDNDYGRAVDWWGLGVVMYEMMCGRLPFYQNDHERLF : 359  
Akt-3 : KIVYRDLKLENMLDKDGHIKITDFGLCKEGITDAATMKTCGTPEYLAPEVLEDNDYGRAVDWWGLGVVMYEMMCGRLPFYQNDHEKLF : 355

Akt-1 : ELILMEEIRFPRTLCPPEAKSLLSGLLKKDPKQRLGGGSEDAKEIMQHRFFAGVWQHIVYEKKLSPPEKPOVTSETDTRYFDEEFTAQMIT : 448  
Akt-2 : ELILMEEIRFPRTLSPPEAKSLLAGLLKKDPKQRLGGGSDAKEVMEHRRFLSINQDVAQKLLPPPEKPOVTSEVDTRYFDDDEFTAQSIIT : 449  
Akt-3 : ELILMEDIKFPRTLSSDAKSLLSGLLJKDPNKRLLGGGPDDAKEIMRHSFFSGANWQDVYDKKLVPPPEKPOVTSETDTRYFDEEFTAQITIT : 445

Akt-1 : ITPPDQDDSD--MEQVDSERRPHFPQFSYASGTA : 480  
Akt-2 : ITPPDYDS--LGLLELDORHFPQFSYASIRE : 481  
Akt-3 : ITPPEKYDEDGMDQMDNERRPHFPQFSYASGRE : 479

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